

REMARKS

The Office Action dated August 28, 2002 has been received and reviewed. Claims 1, 4-7, 11-17 and 23-36 are pending in the present application. All claims stand rejected. The application is to be amended as previously set forth. All amendments and claim cancellations are made without prejudice or disclaimer. As required by 37 C.F.R. § 1.121, a version of the amended claims with markings to clearly show the changes made is attached. Reconsideration is respectfully requested in view of the amendments and remarks herein.

**Second Preliminary Amendment**

Applicants note the filing of a Second Preliminary Amendment on October 23, 2001 which Amendment has not been made of record in the present application. Applicants hereby request entry of the Second Preliminary Amendment. If the Amendment failed for some reason, please so advise and applicants will furnish a true and correct copy to the Examiner. Inadvertently, applicants also did not take into account the amendments made in the October 23, 2001 Second Preliminary Amendment when submitting the June 19, 2002 Amendment (Paper No. 10). In an effort to clarify the pending claims in light of this inadvertent error, any and all amendments made in the Second Preliminary Amendment are also made in the present communication. The number of the amendment stated prior to each claim reflects the Preliminary Amendment filed July 25, 2001, the Second Preliminary Amendment filed October 23, 2001, Paper No. 10 and the present communication. Applicants apologize for any inconvenience this inadvertent error may have caused.

**Rejections Based on Xiang et al.**

Claims 1, 4-7, 11 and 12 have been rejected under 35 U.S.C. § 102(b) as being anticipated by Xiang et al. (1994, *Molecular Cloning and Expression of Alternatively Splice PITSLRE Protein Kinase Isoforms*, Journal of Biological Chemistry, Vol. 269, No. 22, pp. 15,786-15,794) ("Xiang"). Further, claims 13-15, 17, 23 and 24 have been rejected under 35 U.S.C. § 103(a) as being unpatentable over Xiang. Applicants respectfully traverse the rejections as set forth herein.

Xiang discloses that multiple mRNAs may be transcribed from multiple duplicated genes and that, due to alternative splicing events, these transcripts may be translated into PITSLRE protein kinase isoforms ranging in size from 50 to 110 kDa. Most of the resulting isoforms contain the p58<sup>GTA</sup> open reading frame (ORF) and p58<sup>GTA</sup> activity appears to be involved.

In contrast, as amended herein, independent claim 1 recites a recombinant nucleotide sequence enabling a G2/M cell cycle-dependent initiation of translation of mRNA, wherein the recombinant nucleotide sequence is an internal ribosomal entry site (IRES) sequence which initiates mRNA translation in a eukaryotic cell. As amended herein, independent claim 4 recites a recombinant nucleic acid molecule encoding at least a functional part of an eukaryotic IRES, the site (in a mitotic PITSLRE protein kinase gene) comprising SEQ ID NO:1 or a functional part of SEQ ID NO:1, wherein the eukaryotic IRES initiates mRNA translation in a eukaryotic cell.

It is stated in the outstanding Office Action that the Xiang structure “has all the features required to perform the intended use recited in the claims” and that the “function of initiating mRNA translation at an IRES site in a eukaryotic cell is an inherent property of the sequence taught by” Xiang. *Official Action*, page 3, ¶ 4. It is thus asserted that applicants are merely claiming “a new use, new function, or unknown property” of a known sequence which is inherently present in the prior art. *Id.* Applicants respectfully traverse this assertion.

The claims of the present application are generally directed to a specific recombinant sequence, denominated as an internal ribosomal entry site (IRES) sequence, which enables cell-cycle dependent mRNA translation in a eukaryotic cell. This sequence is derived from the p58 and p110 PITSLRE kinases and is defined structurally by the specification of the present application as comprising, at a minimum, SEQ ID NO:7. *Specification*, ¶ [0031]. Thus, applicants are not claiming a “new use, new function, or unknown property” of a known sequence as asserted in the outstanding Office Action but rather are claiming a recombinant fragment derived from a known sequence which has a specific, defined function.

It is asserted in the outstanding Office Action that because Xiang discloses isolated p110 and p58 PITSLRE kinase isoforms, the fragments claimed by the applicants are not novel and unobvious. However, if one were to follow this reasoning, it is respectfully submitted that once a particular

chromosome has been disclosed, all genes present on that chromosome have also been specifically disclosed. Surely this is not the position intended to be asserted.

Accordingly, applicants respectfully submit that independent claims 1 and 4 are both novel and nonobvious over the Xiang reference and respectfully request the withdrawal of the rejections thereof. Claims 5, 6 and 7 depend from claim 4 and, thus, Xiang does not anticipate nor render obvious these claims for at least the above-stated reasons. Thus, applicants respectfully request withdrawal of the rejections of these claims as well.

Claims 11, 12 and 14 recite a chimeric gene, a vector and a eukaryotic host cell, respectively, including (at least) the recombinant nucleotide sequence of claim 1. It is respectfully submitted that Xiang does not teach or suggest the use of chimeric genes, vectors, or eukaryotic host cells containing, in part, the recombinant nucleotide sequence of claim 1 for at least the reasons stated above with regard to the sequence. That is, because the recombinant nucleotide sequence of claim 1 is novel and nonobvious for the above-stated reasons, the chimeric gene, vector and eukaryotic host cell of claims 11, 12 and 14, respectfully, which contain the novel and nonobvious recombinant sequence are both novel and nonobvious as well. Thus, applicants respectfully request withdrawal of the rejections of claim 11, 12 and 14 based upon Xiang. Claims 23 and 24 depend from claim 11, claim 13 depends from claim 12 and claim 15 depends from claim 14. Accordingly, Xiang does not anticipate nor render these claims obvious for at least the above-stated reasons as well.

For at least these reasons, the rejections of claims 1, 4-7 and 11-15, 23 and 24 are believed to be overcome, and the claims are believed to be in condition for allowance. Such favorable action is respectfully requested. Claim 17 has been canceled by way of the present amendment and, thus, the 35 U.S.C. §103(a) rejection of this claim based upon Xiang has been rendered moot.

Each of claims 1, 4-7, 11-15, 23 and 24 are believed to be in condition for allowance and such favorable action is respectfully requested.

**Rejections Based on 35 U.S.C. §112, first paragraph**

Claims 16, 17 and 26 have been rejected under 35 U.S.C. §112, first paragraph, for lack of enablement. Each of claims 16, 17 and 26 have been canceled by way of the present amendment and, thus the rejection of these claims has been rendered moot.

**Rejections Based on Gururajan et al.**

Claims 25 and 27–36 have been rejected under 35 U.S.C. § 103(a) as being unpatentable over Gururajan et al. (1998, *Duplication of a Genomic Region Containing the Cdc2L1-2 and MMP21-22 Genes on Human Chromosome 1p36.3 and their Linkage to D1Z2*, Genome research, Vol. 8, No. 9, pp. 929-939) (“Gururajan”). Applicants respectfully traverse this rejection for the below-stated reasons.

Gururajan discloses that the p36.3 region of human chromosome 1 consists of two identical genomic regions, each of which contain a *Cdc2L* gene linked to a metalloprotease (MMP) gene in a tail-to-tail configuration. It further discloses that the products of the *Cdc2L* genes encode PITSLRE kinases.

By way of contrast, claim 25, as amended herein, recites a recombinant nucleic acid molecule selected from the group consisting essentially of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, or combinations thereof, the nucleic acid molecule initiating the translation of mRNA in a eukaryotic cell.

For the reasons stated above with regard to Xiang, applicants respectfully submit that the disclosure by Gururajan of a gene encoding a PITSLRE kinase does not anticipate the recombinant nucleotide fragments claimed by applicants. Applicants are claiming a recombinant fragment consisting essentially of SEQ ID NO:4, SEQ ID NO:5, or SEQ ID NO:6, the fragment having a specific, defined function. As discussed above, the generic disclosure of the sequence from which the particular recombinant fragments are derived does not anticipate the recombinant fragments having the specific defined functionality. Thus, applicants respectfully request withdrawal of the rejection of claim 25.

Claims 27, 28 and 30 recite a chimeric gene, a vector and a eukaryotic host cell, respectively, comprising, at least in part, the recombinant nucleic acid molecule of claim 25. It is respectfully submitted that Gururajan does not teach or suggest the use of chimeric genes, vectors, or eukaryotic host cells containing, in part, the recombinant nucleotide sequence of claim 25 for at least the reasons stated above with regard to the sequence. That is, because the recombinant nucleotide sequence of claim 25 is novel and nonobvious for the above-stated reasons, the chimeric gene, vector and eukaryotic host cell of claims 27, 28 and 30, respectively, which contain the novel recombinant sequence are novel as well. Thus, applicants respectfully request withdrawal of the rejections of claim 27, 28 and 30 based upon Gururajan. Claim 29 depends from claim 28 and thus claim 28 is believed to be novel for at least the above-cited reasons. As such, applicants respectfully request withdrawal of the rejection of claim 29.

Claim 31 recites an expression system comprising the eukaryotic host cell of claim 30. Claims 32 and 33 recite a vector comprising at least the chimeric gene of claim 27, claim 34 recites a eukaryotic host cell comprising the chimeric gene of claim 27 and claim 35 recites an expression system comprising the eukaryotic host cell of claim 34. Claim 36 recites an expression system comprising the eukaryotic host cell of claim 24. Each of these claims are believed to be novel for at least the above-stated reasons as well. As such, applicants respectfully request withdrawal of the rejections thereof.

Each of claims 25 and 27–36 are believed to be in condition for allowance and such favorable action is respectfully requested.

Serial No.: 09/915,060

CONCLUSION

In view of the amendments and remarks, the claims are believed to be in condition for allowance and an early notice thereof is respectfully solicited. Should the Examiner determine that additional issues remain which might be resolved by a telephone conference, the Examiner is invited to contact applicants' attorney at the address or telephone number given herein.

Respectfully submitted,

A handwritten signature in black ink, appearing to read 'Allen C. Turner', written in a cursive style.

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ACT/TLW/



## VERSION OF CLAIMS WITH MARKINGS TO SHOW CHANGES MADE

Claims 16, 17 and 26 have been cancelled.

Claims 1, 4-7, 11, 12, 14 and 25-28 have been amended as follows:

1. (Three Times Amended) ~~An isolated and/or~~A recombinant nucleotide sequence enabling a G2/M cell ~~cycle-dependent~~cycle-dependent initiation of translation of mRNA, wherein said ~~isolated or~~ recombinant nucleotide sequence is an internal ribosomal entry site sequence which initiates mRNA translation in a eukaryotic cell.

4. (Three Times Amended) ~~An isolated and/or~~A recombinant nucleic acid molecule encoding at least a functional part of ~~an~~a eukaryotic internal ribosomal entry site, which said eukaryotic internal ribosomal entry site, in a mitotic PITSLRE protein kinase gene, comprises SEQ ID NO:1 or a functional part of SEQ ID NO:1 and wherein said eukaryotic internal ribosomal entry site initiates mRNA translation in a eukaryotic cell.

5. (Amended) The ~~isolated and/or~~ recombinant nucleic acid molecule of claim 4 wherein said eukaryotic internal ribosomal entry site is a functional part of SEQ ID NO: 1, said functional part of SEQ ID NO: 1 comprising SEQ ID NO: 7.

6. (Amended) The ~~isolated and/or~~ recombinant nucleic acid molecule of claim 4 further comprising at least a part of SEQ ID NO: 1 or a nucleotide sequence at least substantially homologous to SEQ ID NO: 1.

7. (Twice Amended) The ~~isolated and/or~~ recombinant nucleic acid molecule of claim 4, wherein said ~~isolated and/or~~ recombinant nucleic acid molecule comprises at least a part of SEQ ID NO:1 sufficient to encode a functional part of a eukaryotic internal ribosomal entry site, a sequence hybridizing under conventional conditions to at least a part of SEQ ID NO:1 sufficient to encode a said functional part of a said eukaryotic internal ribosomal entry site, or a complementary sequence of

SEQ ID NO:1, said complementary sequence encoding asaid functional part of asaid eukaryotic internal ribosomal entry site.

11. (Four Times Amended) A chimeric gene comprising:

(a) ~~the isolated and/or~~said recombinant nucleotide sequence of claim 1, and

(b) one or more control sequences operably linked to said ~~isolated and/or~~ recombinant nucleotide sequence.

12. (Four Times Amended) A vector comprising the ~~isolated and/or~~ recombinant nucleotide sequence of claim 1.

14. (Four Times Amended) A eukaryotic host cell comprising the recombinant nucleotide sequence of claim 1.

25. (Amended) ~~An isolated and/or~~A recombinant nucleic acid molecule selected from the group consisting essentially of SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, or combinations thereof, said recombinant nucleic acid molecule initiating the translation of mRNA in a eukaryotic cell, ~~said nucleic acid molecule initiating the translation of mRNA in a eukaryotic cell.~~

27. (Amended) A chimeric gene comprising:

a) the ~~isolated and/or~~ recombinant nucleic acid molecule of claim 25, and

b) one or more control sequences operably linked to said ~~isolated and/or~~ recombinant nucleic acid molecule.

28. (Amended) A vector comprising the ~~isolated and/or~~ recombinant nucleic acid molecule of claim 25.